

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2u model

Run on: January 16, 2003 16:55:57 ; Search time 1144 56 seconds
(without alignments)
330.553 Million cell updates/sec

Title: US-09-856-070-19
Perfect score: 65
Sequence: 1 KEELMLRLQDVEE 13

Scoring table: BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2354640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match: 0%
Maximum Match: 100%
Listing first 45 summaries

Command line parameters: -DEV-xlp
-O/cgpn2.1/USPTO.spool/US09856070/runat_14012003_155834_1621/app_query.fasta_1.1592
-De-GenEmbl -QEXT=fastap -SUPER=1 -MINMATCH=0.1 -LONG=1 -G -L -E -P -T -O
-UNITS=bills -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DUALALIGN=200 -THR_SCORE=pcr -THR_WAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09856070 -G3CN_1_15791_9/runat_14012003_155834_1621 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NP2_SCORES=0 -WAIT -L=0 -T=0 -DPV -TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-Ygapop=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:
1: gb_ha.*
2: gb_hfq.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_rf.*
10: gb_ro.*
11: gb_sl.*
12: gb_st.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fus.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_on.*
21: em_or.*
22: em_ox.*
23: em_pal.*
24: em_ph.*
25: em_pi.*
26: em_ro.*
27: em_st.*
28: em_un.*

29: em_vi.*
30: em_hfq_hum.*
31: em_hfq_inv.*
32: em_hfq_other.*
33: em_hfq_mus.*
34: em_hfq_pln.*
35: em_hfq_rod.*
36: em_hfq_mam.*
37: em_hfq_vrt.*
38: em_sy.*
39: em_hfqo_hum.*
40: em_hfqo_mus.*
41: em_hfqo_other.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | LB | IL | Description |
|------------|-------|---------------|--------|----|----|-------------------|
| 1 | 65 | 100.0 | 2514 | 4 | 4 | BOVE2PINA |
| 2 | 65 | 100.0 | 2930 | 9 | 9 | HEMVIL2 |
| 3 | 65 | 100.0 | 3044 | 6 | 6 | AX411074 Sequence |
| 4 | 65 | 100.0 | 3044 | 9 | 9 | HSE2RIN |
| 5 | 65 | 100.0 | 3047 | 6 | 6 | AX440476 Sequence |
| 6 | 65 | 100.0 | 3072 | 9 | 9 | HSM8992625 |
| 7 | 65 | 100.0 | 3173 | 9 | 9 | BE013903 |
| 8 | 65 | 100.0 | 215705 | 9 | 9 | AL589931 |
| 9 | 62 | 95.4 | 478 | 9 | 9 | AF189213 |
| 10 | 62 | 95.4 | 2701 | 10 | 10 | NME2K |
| 11 | 62 | 95.4 | 183302 | 2 | 2 | ACU87605 |
| 12 | 62 | 95.4 | 387782 | 2 | 2 | ACG74334 |
| 13 | 62 | 95.4 | 317417 | 2 | 2 | ACG23429 |
| 14 | 62 | 95.4 | 286508 | 2 | 2 | ACL25143 |
| 15 | 60 | 92.3 | 475 | 9 | 9 | AF188897 |
| 16 | 58 | 89.2 | 1446 | 10 | 10 | AF450298 |
| 17 | 58 | 89.2 | 189873 | 2 | 2 | AC125736 |
| 18 | 53 | 81.5 | 182330 | 2 | 2 | AC118744 |
| 19 | 50 | 76.9 | 426 | 4 | 4 | AF199015 |
| 20 | 50 | 76.9 | 2545 | 5 | 5 | AB019790 |
| 21 | 44 | 67.7 | 2790 | 1 | 1 | SAPNTPASE |
| 22 | 44 | 67.7 | 4875 | 1 | 1 | SAC437617 |
| 23 | 44 | 67.7 | 113552 | 9 | 9 | AC105419 |
| 24 | 44 | 67.7 | 177263 | 8 | 8 | AF030376 |
| 25 | 44 | 67.7 | 184415 | 2 | 2 | AC011226 |
| 26 | 44 | 67.7 | 187981 | 2 | 2 | AC014786 |
| 27 | 44 | 67.7 | 209170 | 2 | 2 | AL731686 |
| 28 | 43 | 46.2 | 2589 | 5 | 5 | AF342739 |
| 29 | 43 | 56.2 | 77132 | 2 | 2 | AF033820 |
| 30 | 43 | 66.2 | 143794 | 8 | 8 | AP004305 |
| 31 | 43 | 66.2 | 15419 | 2 | 2 | AC064662 |
| 32 | 43 | 66.2 | 204285 | 2 | 2 | AB005425 |
| 33 | 42 | 64.6 | 471 | 9 | 9 | AF188896 |
| 34 | 42 | 64.6 | 489 | 9 | 9 | AF187552 |
| 35 | 42 | 64.6 | 89494 | 9 | 9 | AC005024 |
| 36 | 42 | 64.6 | 116468 | 9 | 9 | AC099568 |
| 37 | 42 | 64.6 | 119481 | 9 | 9 | AL136234 |
| 38 | 42 | 64.6 | 1241 | 9 | 9 | AC004543 |
| 39 | 42 | 64.6 | 157107 | 2 | 2 | AC000642 |
| 40 | 42 | 64.6 | 160664 | 2 | 2 | AC004190 |
| 41 | 42 | 64.6 | 178064 | 2 | 2 | AC023311 |
| 42 | 42 | 64.6 | 178157 | 2 | 2 | AC130436 |
| 43 | 42 | 64.6 | 181320 | 2 | 2 | AC006303 |
| 44 | 42 | 64.6 | 182795 | 2 | 2 | AF004891 |
| 45 | 42 | 64.6 | 183965 | 9 | 9 | AC068764 |

ALIGNMENTS

RESULT 1

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-070-19 (1-13) x AX411074 (1-3044)

QY 1 LysGluGluLeuMetLeuArgLeuGlnAspTyrGluGlu 13
|||||
DB 1147 AAGGAGGACTTCATCCCTCCCTCCAGGACATATGAGGAG 1185

RESULT 4

HSEZRIN 3044 bp mRNA linear PRI 12-SEP-1993
LOCUS Human mRNA for ezrin.

DEFINITION X51521
ACCESSION X51521 1 GI:31282
VERSION ezrin; kinase substrate; microvilli protein.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.

ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3044)
AUTHORS Hunter, T.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-1990) Hunter T., The Salk Institute, Molecular
Biology and Virology Laboratory, 10010 North Torrey Pines Road, San
Diego, CA 92138, USA

REFERENCE 2 (bases 1 to 3044)
AUTHORS Gould, K.L., Bretscher, A., Esch, F.S. and Hunter, T.
TITLE cDNA cloning and sequencing of the protein-tyrosine kinase
substrate, ezrin, reveals homology to band 4.1

JOURNAL EMBO J. 8 (13), 4133-4142 (1989)

MEDLINE 90076135
PubMed 2591371

COMMENT: See also 3050215.
FEATURES
source location/Qualifiers
1..3044
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="F6"
/cell_line="HeLa"
/clone_lib="Okayama-Herg"
118 1878
/note="ezrin (AA 1-586)"
/codon_start=1
/protein_id="CAA35893.1"
/db_xref="GI:31283"
/db_xref="SWISS-PROT:P15311"
/translation="MPKPIWVRVTMDAELEFATQPTNTT-KOLFTQVVKVTKLPEFVWY
ENIHYVANKGPEPTWFLKDKVSAGEVPEKRNPIQFKEPAKFTYEDVAEELIQDITQFLF
FLVKEGILSDIYCPETAVILGSAVQAKFGYNNKFKVSKYLSSERLTPQRYWQ
HKILRDWEDRIQWHAHRCMIKINAMIPYIKIADLPMTGINTFEIKKKGIDW
GVDAIGLNTYKDKKLTIPKTPGFWSEIPNTSPNKKFVPIPIKKAPDVFYAPKPI
NKRILQICMGNHILYMKRRKDDITFVQOMKAQAREKHQKQLERQOLTPKKRRTVE
REKQMRKREFEIMRLQDYEEKTKAEARELSQIQALQLEERKRAQEEAEARLEAD
RMAALAKKEELQVADQIKSQEOLAAELAEYIAKIALLEAARKEDEVEEMOHRAK
EAQDLVKTEELHLYMTAPPVPPVPSVGVGSELSQRCAPTGYSAELSEGI
KDDNFKRITAEKKNRQVQIVTLSSRLSQARDENKKIHNILHNENMKRCKRYK
TIRIQRCNKTQRIDRPEAL."

old_sequence 1709..1711
/note="tcg was tgc in [1]"
/citation=[1]

BASE COUNT 826 a 687 c 855 g 675 t 1 others

ORIGIN

Alignment Scores:
Pred. No.: 0.000857 Length: 3044
Score: 65.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-856-070-19 (1-13) x HSEZRIN (1-3044)

QY 1 LysGluGluLeuMetLeuArgLeuGlnAspTyrGluGlu 13
|||||
DB 1147 AAGGAGGACTTCATCCCTCCCTCCAGGACATATGAGGAG 1185

RESULT 5

LOCUS AX440476 3047 bp DNA linear FAT 28 JUN 2002
DEFINITION Sequence 329 from Patent WO0190154.
ACCESSION AX440476
VERSION AX440476.1 GI:21665286
KEYWORDS human.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Xu, J., Mitcham, J.L., Harlocker, S.L., Dillon, D.C., Secrist, H.,
Lodes, M.J., Algate, P.A., Fling, S.P., Mannion, J.F., Benson, D.R. and
Carter, D.
TITLE Compositions and methods for the therapy and diagnosis of ovarian
cancer
JOURNAL Patent: WO 0190154-A 329 29-NOV-2001;
COPRIX COPPERATION (US)
FEATURES location/Qualifiers
1..3047
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 828 a 687 c 856 g 675 t 1 others

ORIGIN

Alignment Scores:
Pred. No.: 0.000857 Length: 3047
Score: 65.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-070-19 (1-13) x AX440476 (1-3047)

QY 1 LysGluGluLeuMetLeuArgLeuGlnAspTyrGluGlu 13
|||||
DB 1147 AAGGAGGACTTCATCCCTCCCTCCAGGACATATGAGGAG 1185

RESULT 6

LOCUS HSM802625 4072 bp mpna linear FBI 23 MAR-2000
DEFINITION Homo sapiens mpna; cDNA DKFZ762H157 (from clone DKFZ762H157);
complete cds.
ACCESSION AL162086
VERSION AL162086.1 GI:7428174
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.

ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4072)
AUTHORS Ottenwälder, B., Gbermaier, B., Mewes, H.W., Weil, H. and Wiemann, S.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2000) MIPS, Am Klefierspitz 16a, D-82152
Martinsried GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by MedGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZ762H157) is available at the R2PD in Berlin. Please contact
the R2PD, Postfach 50000, D-10509
Berlin-Charlottenburg, GERMANY, Email: charlotten@r2pd.de for further
information about the clone and the sequencing project is available
at <http://www.mips.biochem.mpg.de/r2pd/cDNA/>.

FEATURES
source location/Qualifiers
1..3072

US-09-856-070-19 (1-13) x HSEZRIN (1-3044)


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* 187911 190625: contig of 2715 bp in length
* 190626 190645: gap of unknown length
* 190646 192088: contig of 1443 bp in length
* 192089 192198: gap of unknown length
* 192199 193637: contig of 1529 bp in length
* 193638 194657: gap of unknown length
* 194658 195040: contig of 1383 bp in length
* 195041 195060: gap of unknown length
* 195061 196945: contig of 1885 bp in length
* 196946 196965: gap of unknown length
* 196966 198219: contig of 1254 bp in length
* 198220 198239: gap of unknown length
* 198240 199307: contig of 1668 bp in length
* 199308 199927: gap of unknown length
* 199928 201164: contig of 1236 bp in length
* 201165 201183: gap of unknown length
* 201184 202027: contig of 844 bp in length
* 202028 202047: gap of unknown length
* 202048 202902: contig of 855 bp in length
* 202903 202922: gap of unknown length
* 202923 204159: contig of 1228 bp in length
* 204160 204179: gap of unknown length
* 204180 205707: contig of 1537 bp in length
* 205708 205727: gap of unknown length
* 205728 207782: contig of 2055 bp in length.

```

FEATURES

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source
1..207782
/organism="Mus musculus"
/strain="C57BL6/J"
/db_xref="taxon:10090"
/chromosome="15"
/clone="RP23-103120"
/sex="male"
BASE COUNT 54791 a 49882 c 49733 g 53275 t 3101 others
ORIGIN

```

```

Alignment Scores:
Pred. No.: 0.333 Length: 207782
Score: 62.00 Matches: 12
Percent Similarity: 100.00% Conservations: 1
Best Local Similarity: 92.31% Mismatches: 0
Query Match: 95.38% Indels: 0
EB: 2 Gaps: 0

```

```
US-09-856-070-19 (1-13) x AC074334 (1-207792)

```

```

CQ 1 LysGluGluLeuMetLeuArgLeuGlnAspTyrGlnGlu 13
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db 173053 AAGGAGAGGTGATGCTTGCGTGCAGACATACGACAG 173015

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RESULT 13

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AC022329/c 217917 bp DNA linear HTC 15-MAY-2002
LOCUS
DEFINITION Mus musculus clone RP23-103120 strain C57BL6/J, WORKING DRAFT
SEQUENCE, 11 unordered pieces.
AC022329

```

```
AC022329.8 C1:18057360

```

```
HTG; HTGS_PHASE1; HTGS_DRAFT.

```

```
Mus musculus

```

```
Mus musculus

```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```
1 (bases 1 to 217917)

```

```
Montgomery,K.P., Grills,G., Han,J., Lee,P., Long,J., Pomerantsev,P.,

```

```
Ioshikhes,I.P., Shim,C., Becker,J., Thomas,P., Perera,A.,

```

```
Gordon,M., Goltz,J.S. and Kucherlapati,R.

```

```
High Throughput Mouse Sequencing

```

```
Unpublished

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2 (bases 1 to 217917)

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Montgomery,K.P., Grills,G., Han,J., Lee,P., Long,J., Pomerantsev,P.,

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Ioshikhes,I.P., Shim,C., Becker,J., Thomas,P., Perera,A.,

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Gordon,M., Goltz,J.S. and Kucherlapati,R.

```

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Direct Submission

```

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TITLE

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JOURNAL

COMMENT

```

Submitted (01-FEB-2003) Department of Molecular Genetics, Albert
Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
Bronx, NY 10461, USA
On Jan 4, 2002 this sequence version replaced gi:11094413.
-----
Center: Harvard Partners Genome Center
Center Code: HPGC
Web site: http://www.hpgc.org/Sequence/mouse.html
Contact: hpgcmodel.mgh.harvard.edu
-----
-----Summary Statistics
Center project name: AAC
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 100%
*Consensus quality: 212564 at least Q20
*Consensus quality: 211720 at least Q30
*Consensus quality: 210397 at least Q40
Estimated insert size: agarose-pp - N/A
**Estimated insert size: 217717 - sum-of-connigs
Quality coverage: agarose-pp - N/A
Quality coverage: 8.5 x in Q20 bases; sum-of-connigs estimation
-----

```

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs, the true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

1 60900: contig of 60900 bp in length
* 60901 60920: gap of unknown length
* 60921 106520: contig of 45600 bp in length
* 106521 106540: gap of unknown length
* 106541 142322: contig of 35782 bp in length
* 142323 142342: gap of unknown length
* 142343 176177: contig of 33835 bp in length
* 176178 176197: gap of unknown length
* 176198 204272: contig of 28075 bp in length
* 204273 204292: gap of unknown length
* 204293 209253: contig of 4960 bp in length
* 209254 209273: gap of unknown length
* 209274 214332: contig of 5060 bp in length
* 214333 214352: gap of unknown length
* 214353 215731: contig of 1379 bp in length
* 215732 215751: gap of unknown length
* 215752 215800: contig of 49 bp in length
* 215801 215820: gap of unknown length
* 215821 216675: contig of 855 bp in length
* 216676 216695: gap of unknown length
* 216696 217917: contig of 1222 bp in length.

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FEATURES

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source
1..217917
/organism="Mus musculus"
/strain="C57BL6/J"
/db_xref="taxon:10090"
/clone="RP23-103120"
/sex="male"
1..60900
/feature="assembly_name:Contig211"
60921..106520
/feature="assembly_name:Contig210"
106541..142322
vector_side:left"
142343..176177
/feature="assembly_name:Contig209"
176198..204272
/feature="assembly_name:Contig208"
204293..209253
vector_side:left"
209274..214332
/feature="assembly_name:Contig207"
214353..215731
/feature="assembly_name:Contig206"

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misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

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misc_feature      292973      214332
                  /note="assembly_name:Contig205"
misc_feature      214353      215731
                  /note="assembly_name:Contig204"
misc_feature      215752      215800
                  /note="assembly_name:Contig203"
misc_feature      215821      215675
                  /note="assembly_name:Contig202"
misc_feature      216096      217417
                  /note="assembly_name:Contig201"
BASE COUNT      59698 a 52987 c 49774 g 5541 t
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| Prepared, No.: | 0.351 | length: | 217917 |
| Score: | 62.00 | Matches: | 12 |
| Percent Similarity: | 100.00% | Conservative: | 1 |
| Best Local Similarity: | 92.31% | Mismatches: | 0 |
| Query Match: | 95.38% | Indels: | 0 |
| EB: | 2 | Gaps: | 0 |

US-09-856-070-19 (1-13) x AC022329 (1-217917)

409 1 LysC(L)GfLpLpMetLeuArgLeuLpASpGyrGluChLp 13

10735 AACGAGGAGCTGATGCTTGGCTTGAAGATATGAAATAG 10697

| | | | | |
|------------|---|-----|-------|-----------------|
| RESULT 14 | | | | |
| AC125143/c | | | | |
| LOCUS | 286508 bp | UNA | 1:ear | BIC 98-AUG-2392 |
| DEFINITION | MUS MUSCULUS CHROMOSOME 71NK clone PP24-342113, WORKING DRAFT | | | |
| | SEQUENCE 10 unordered pieces. | | | |

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

- * NOTE: This is a 'working draft' sequence. It currently
- * consists of 10 runs iqs. The true order of the pieces

```

VERSION      AF188897.1  GI:6063144
KEYWORDS
SOURCE
ORGANISM      Homo sapiens.
               Homo sapiens
               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 475)
AUTHORS      Chen,Z.C., Fadiel,A. and Naittolin,F.
TITLE        Ezrin gene mutation in ovarian cancer
JOURNAL
REFERENCE    2 (bases 1 to 475)
AUTHORS      Chen,Z.C., Fadiel,A. and Naittolin,F.
TITLE        Direct Submission
JOURNAL      Submitted (22-SEP-1999) DB/GEN, Yale University, 333 Cedar Street,
               New Haven, CT 06511, USA
FEATURES
SOURCE
1..475
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   /db_xref="taxon:9606"
   /chromosome="6"
   /map="6q22-q27"
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   /col_type="epithelial cancer cells"
   /tissue_type="ovary"
   <1..3475
   /note="villin 2; kinase substrate"
   /codon_start=2
   /product="ezrin"
   /protein_id="AAF03155.1"
   /db_xref="GI:6063145"
   /translation="TSMYGINYFEVKNKKGTLWI.GVDALGLNIYEKDDKLPKIGEP
WSEIRTSNDKKFVKPIDKKAPDFVYAPGLRINKRTIALCMGNHLYMRPRKPD
IEVQWKAARFAHKKQLERQQLEFAKKKKKVFKKKKQMMPEKEFLMKLQDYF"
BASE COUNT   154 a   90 c   136 g   93 t
ORIGIN
Alignment Scores:
Pred. No.:      0.00136      Length:      475
Score:          60.00      Matches:      12
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:     92.31%      Indels:      0
Db:              9      Gaps:      0

US-09-856-070-19 (1-13) x AF188897 (1-475)
QY      1  LysGlnGlnLeuMetLeuArgLeuGlnAspTyrGlu 12
        |||||||
Db      440 AAGGAGGAGTTCATGCTCGGCTCGAGGACTATGAA 475

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Search completed: January 16, 2003, 19:03:44
Job time : 1208.56 secs